

GCTCTCCCTGCTCCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTG  
M R A L E G P G L S L L  
 TGCCTGGTGTGGCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAA  
C I V L A L P A L L P V P A V R G V A E  
 ACACCCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGGCTGGTGTGCGCCCGAGTGC  
 T P T Y P W R D A E T G E R L V C A Q C  
 CCCCCAGGCACCTTGTGCAGCGGCCGTGCCGCCAGACAGCCCCACGACGTGTGGCCCG  
 P P G T F V Q R P C R R D S P T T C G P  
 TGTCACCGCGCCACTACACGCAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAAC  
 C P P R H Y T Q F W N Y L E R C R Y C N  
 GTCCCTCTGGGGGAGCGTGAGGAGGAGGCACGGGCTGCCACGCCACCCACAACCGTGCC  
 V L C G E R E E E A R A C H A T H N R A  
 TGCCGCTGCCGCACCGGCTTCTCGCGCACGCTGGTTCTGCTGGAGCACGCATCGTGT  
 C R C R T G F F A H A G F C L E H A S C  
 CCACCTGGTGCCGGCGTATTGCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCG  
 P P G A G V I A P G T P S Q N T Q C Q P  
 TGCCCCCCCAGGCACCTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGC  
 C P P G T F S A S S S S S E Q C Q P H R  
 AACTGCACGGCCCTGGCCTGGCCCTCAATGTGCCAGGCTCTCCCTCCATGACACCCCTG  
 N C T A L G L A L N V P G S S S H D T L  
 TGCACCAGCTGCACTGGCTCCCCCTCAGCACCAAGGGTACCAAGGAGCTGAGGAGTGTGAG  
 C T S C T G F P L S T R V P G A E E C E  
 CGTGCCGTATCGACTTTGTGGCTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTG  
 R A V I D F V A F Q D I S I K R L Q R L  
 CTGCAGGCCCTCGAGGCCCGGAGGGCTGGGCTCCGACACCAAGGGCGGGCCGCGCGGCC  
 L Q A L E A P E G W G P T P R A G R A A  
 TTGCAGCTGAAGCTGCGTCGGCGCTCACGGAGCTCTGGGGCGCAGGACGGGCGCTG  
 L Q L K L R R R L T E L L G A Q D G A L  
 CTGGTGCAGCTGCACTGAAAGAGGCTTTTTAAATAGAAGAAATGAGGTTCTAAAG  
 L V R L L Q A L R V A R M P G L E R S V  
 CGTGAGCGCTTCCCTGTGCACTGATCCTGGCCCCCTCTTATTATTCTACATCCTTG  
 R E R F L P V H \*  
 GCACCCCACTTGCACTGAAAGAGGCTTTTTAAATAGAAGAAATGAGGTTCTAAAG  
 CTTATTTTATAAGCTTTTCTAAAAAaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

FIG.1

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TGGCATGTCGGTCAGGCACAGCAGGGTCTGTGTCCCGCCTGAGCCGCGCTCTCCCTGCT  
CCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGTGCCTGGTGTG  
M R A L E G P G L S L L C L V L  
GCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTAC  
A L P A L L P V P A V R G V A E T P T Y  
CCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCACCCCCAGGCACC  
P W R D A E T G E R L V C A Q C P P G T  
TTTGTGCAGCGGCCGTGCCGCCAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGC  
F V Q R P C R R D S P T T C G P C P P R  
CACTACACGCAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCCCTGCGGG  
H Y T Q F W N Y L E R C R Y C N V L C G  
GAGCGTGAGGAGGAGGCACGGCTTGCCACGCCACCAACCGTGCCTGCCGCTGCCGC  
E R E E E A R A C H A T H N R A C R C R  
ACCGGCTTCTCGCGCACGCTGGTTCTGCTTGAGCACGCATCGTGTCCACCTGGTGCC  
T G F F A H A G F C L E H A S C P P G A  
GGCGTGATTGCCCGGGTGAGAGCTGGCGAGGGAGGGGCCAGGAGTGGTGGCG  
G V I A P G E S W A R G G A P R S G G R  
AGGTGTGGCAGGGTCAGGTTGCTGGTCCAGCCTGACCCCTGAGCTAGGACACCAGTT  
R C G R G Q V A G P S L A P \*  
CCCCCTGACCCCTGTTCTCCCTCCTGGCTGCAGGCACCCCCAGCCAGAACACGCAGTGCCA  
GCCGTGCCCGAGGCACCTCTCAGCCAGCAGCTCCAGCTAGAGCAGTGCCAGCCCCA  
CCGCAACTGCACGGCCCTGGCCTGCCCTCAATGTGCCAGGCTTCCCTCCATGACAC  
CCTGTGCACCAGCTGCACTGGCTCCCCCTCAGCACCAAGGTACCAAGGTGAGCCAGAGG  
CTGAGGGGGCAGCACACTGCAGGCCAGGCCACTTGTGCCCTCACTCCTGCCCTGCACG  
TGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGAAAGGGGCCACAGTGGATTGAGGG  
TCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCTCTCAGGGTGGCTGAGAATT  
GGATCTGAGCCAGGGCACAGCCTCCCTGGAGAGCTCTGGAAAGTGGCAGCAATCTCC

FIG.2A

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TAACTGCCGAGGGGAAGGTGGCTGGCTCCTCTGACACGGGAAACCGAGGCCTGATGGT  
AACTCTCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTGACATGGGAAACCGAGGC  
CCAATGTTAACCACTGTTGAGAAGTCACAGGGGAAGTGACCCCTTAACATCAAGTCAG  
GTCCGGTCCATCTGCAGGTCCAACTCGCCCCCTCCGATGGCCCAGGAGCCCCAAGCCCT  
TGCCTGGGCCCCCTGCCTCTGCAGCCAAGGTCCGAGTGGCCGCTCTGCCCCCTAGGC  
CTTGCTCCAGCTCTGACCGAAGGCTCCTGCCCTCTCCAGTCCCCATGTTGCACT  
GCCCTCTCCAGCACGGCTCACTGCACAGGGATTCTCTCTGCCAGTCCAAACCCCCCGAGTGG  
GGCCCAGAAAGCAGGGTACCTGGCAGCCCCGCCAGTGTGTGGGTGAAATGATCGGAC  
CGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAGTGTGAGCGTGCCGTATCGACTTG  
TGGCTTCCAGGACATCTCCATCAAGAGGAGCGGCTGCTGCAGGCC

**FIG.2B**

M	- G	L	S	T	V	P	D	L	L	P	L	V	L	E	L	L	V	G	I	Y	P	S	G	V	I	G	L	V	H	L	G	D	R	E	-	TNFR1							
M	A	P	V	A	V	W	A	A	M	D	-	G	P	R	L	L	L	W	A	A	H	A	H	A	L	P	A	Q	V	A	-	-	F	T	P	-	-	TNFR2					
M	G	A	G	A	T	G	A	M	R	A	M	-	R	L	P	R	-	G	P	C	G	L	A	W	G	P	L	L	G	L	S	G	V	S	L	G	G	A	K	E	-	-	NGFR
M	L	G	T	W	T	-	L	P	L	V	L	-	L	P	L	V	L	T	S	V	-	A	R	L	S	S	K	S	V	N	A	Q	V	T	D	I	N	S	K	G	L	FAS	
M	R	V	L	P	L	-	A	R	P	H	P	-	W	W	L	C	V	L	G	T	L	V	G	L	S	-	A	T	P	A	P	K	S	C	P	-	-	CD27					
M	N	Y	R	L	P	L	-	Q	-	-	-	-	L	A	A	L	G	L	L	F	L	G	A	L	R	A	-	-	-	F	P	Q	-	-	CD30								
M	C	V	G	A	-	R	R	L	G	-	-	C	V	L	-	W	G	C	L	-	-	T	A	V	H	P	E	-	-	P	P	-	-	CD40									
M	K	S	V	-	L	Y	L	Y	I	-	-	S	C	Y	N	I	V	A	T	L	L	V	L	N	-	-	-	-	F	E	R	-	-	4-1BB									
M	K	S	-	-	Y	I	L	L	-	-	-	R	G	P	C	A	A	L	L	L	G	L	G	L	S	T	V	T	G	L	H	C	V	-	-	OX40							
M	R	A	L	E	-	-	-	-	-	-	-	F	L	S	C	I	I	I	N	G	R	D	A	A	P	-	-	-	Y	T	P	-	-	VC22									
M	R	A	L	E	-	-	-	-	-	-	-	L	L	S	C	I	I	I	N	S	D	I	T	P	-	-	-	H	E	P	-	-	CRMB										
M	R	A	L	E	-	-	-	-	-	-	-	G	P	G	L	S	L	L	C	L	V	L	A	L	P	A	L	P	-	-	-	V	P	A	-	-	TNFR-6a						
M	R	A	L	E	-	-	-	-	-	-	-	G	P	G	L	S	L	L	C	L	V	L	A	L	P	A	L	P	-	-	-	V	P	A	-	-	TNFR-6b						

FIG. 3A

FIG. 3B

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FIG. 3C

FIG. 3D

149	- - -	C L N G T V H L	- - S C Q E K Q N T V C T -	C H A G F F L R E - - -	- - -
141	R - -	C R P G F G V A R P G T E T S D V Y -	C K P C A P G T F S N T T S S T	T D TNFR2	
128	- - -	C E A G S G L V - F S C Q D K Q N T V C E E C P D G T Y S D E A N H V D NGFR	C V P C K P G H F Q N T S S P R A L T b R		
146	R L V L C	C Q P G T E A E V T D E I M D T D Y N C V P C K P G H F Q N T S S P R A L T b R	- - -	- - -	E FAS
137	- - -	C H S G L - L V - R N C T I I A N A E C A - C R N G W -	- - -	- - -	- CD27
87	- - -	C P A G M I V K F P G T A Q K N T Y -	C E P A S P G V - S P A C A S P E CD30		
129	S V - -	C S P G F G V K Q I A T G V S D T I -	C E P C P V G F F S N V S S A F E CD40		
123	R - - -	C K Q G Q E L T K K G - - -	C K D C C F G T F N D Q K R G I - 4-1B		
106	- - -	R A G T Q P L - D S Y - -	C A P C P P G H F S P G D N Q - - 0X40		
110	- - -	C G I G Y G V S G H - T S V G D V I -	C S P C G F G T Y S H T V S S A D VC22		
131	T - -	K C G I G Y G V S G H - T P T G D V V -	C S P C G L G T Y S H T V S S V D CRMB		
131	T - -	- - -	- - -	- - -	
130	A - -	S C P P G A G V I A P G T P S Q N T Q - C Q P C P P G T F S A S S S E TNFR-6a	- - -	- - -	
130	A - -	S C P P G A G V I A P G -	- - -	- - -	- TNFR-6b

FIG.3E

178 E C V S C S N C K - - - - -  
 178 I C R P H Q T C N V Y A - - - - -  
 163 P C L P C T V C E D T E R Q - L R E C T R W A D A E C - - - - -  
 186 R C Q P H T R C E I Q G L V E A P G T S Y S D T I C K N P P E P G A M L L - - - - -  
 142 H C D P C T K C E - - - - -  
 111 Q C R D - K E C T - - - - -  
 165 N C K E P S S G T I P Q - A K P T P V S P A T S S A S T M P V R G G T R L A Q E C D 3 0  
 160 K C H P W T S C E T K D L V V Q Q A G T N K T D V V C G P S P - - - - -  
 133 - C R P W T N C S L D G K S V L V N G T K E R D V V C G P S P - - - - -  
 140 A C K P W T N C T L A G K H T L Q P A S N S S D A I C - - E D - - - - -  
 167 K C E P V P N N T F N Y I D V E I T L Y P V N D T S C T R T T T T - - - - -  
 167 K C E P V P S N T F N Y I D V E I N L Y P V N D T S C T R T T T T - - - - -  
 167 Q C Q P H R N C T A L G L A L N V P G S S H D T L C T S - - - - -  
 143 - - - - -  
 TNFR1 - - - - -  
 TNFR2 - - - - -  
 NGFR - - - - -  
 LTbR - - - - -  
 FAS - - - - -  
 CD27 - - - - -  
 A 4-1BB - - - - -  
 OX40 - - - - -  
 VC22 - - - - -  
 CRMB - - - - -  
 TNFR-6a - - - - -  
 TNFR-6b - - - - -

FIG. 3F

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196 -  
143 -

FIG. 3G

FIG. 3H

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FIG. 3

264	T K P L A P N P S F S	P T P G F T P T L G F S P V P S S T F T S S S T Y T P G D	TNFR1
294	- - - - - L Q R E A K V P H L P A - D K A R G T Q G P E Q Q H L L I T A - -	- - TNFR2	
281	- - - - - N K Q G A N S R P V - N Q T P P P E G E K L H S D S G I S V D	NGFR	
262	- - - - - P E G E E S P P C P A - P R A D P H F D L A E P L L - - -	- - LTbR	
212	- - - - - S P T L N P E - - T V A I N L S D V D L S K Y I T - - -	- - FAS	
169	- -	- - - - - L P CD27	
322	T T F E A P P L G T Q P D C N P T P E - N G E A P A S T S P T Q S L L V D S Q A	CD30	
222	- - - - - P T N K A P H P K Q E - P Q-E I N F P D - - - - - - - - - - -	CD40	
193	- -	- - 4-1B	
198	- - - - - T S Q G P S T R P V - E - - V P G G R A V A A I L G L G L -	0X40	
255	- - - - - L N F E I K C N N - - - - - K G S - - S F K Q - - L T K - -	VC22	
255	- - - - - L N F E I K C N N - - - - - K D S Y S S S K Q - - L T K - -	CRMB	
229	- - - - - L Q R L L Q A L E A P E - G W - - G P - - - - - - - - - - -	- - T - - TNFR-6a	
143	- - - - - - - - - - - E - S W A R G G - - - - - - - - - - - - - - - - -	- - A - - TNFR-6b	

FIG. 3J

304	C P N F A A	P R R E V A P P Y Q G	A D P I L A T A	- - - - -	- - - - -	TNFR1
324	- - - - -	- P S S S S S L E S S A S A L	- - - - -	- - - - -	- - - - -	TNFR2
311	S Q S L H D Q	Q P H T Q T A S G Q A L K	- - - - -	G D G G L Y S S L P P A K R E E	NGFR	
288	- - - - -	- P M S G D L S P S P A G P P T	- - - - -	- - - - -	- - - - -	L T $\beta$ R
236	- - - - -	- - - - -	- - - - -	- U A G V	- - - - -	FAS
171	A R T L S T H W P P Q R S L C S S D F I	- - - - -	- R I L V I F S G M F L V F T L A	CD27		
361	S K T L P I P	P T S A P V A L S S T G K P V L D A G P V L F W V I L V L V V G	CD30			
241	- - - - -	- D L P G S N T A A P V	- - - - -	- - - - -	- - - - -	CD40
193	- - - - -	- A L T S T A L L F L	- - - - -	- L F F L T L R F S V V K R	4-1BB	
224	- - - - -	- - - - -	- V L G L	- - - - -	- G P L A I L L A L Y L L R R D Q	OX40
274	- - - - -	- A K N D D G - M	- - - - -	- - - - -	- - - - -	VC22
276	- - - - -	- T K N D D S I	- - - - -	- - - - -	- - - - -	CRM $\beta$

FIG. 3G

246	- - - - -	- P R A G R A A L Q L K	- - - - -	- - - - -	- - - - -	TNFR-6a
151	- - - - -	- P R S G	- - - - -	- - - - -	- - - - -	TNFR-6b

FIG.3K

FIG. 3

FIG. 3M

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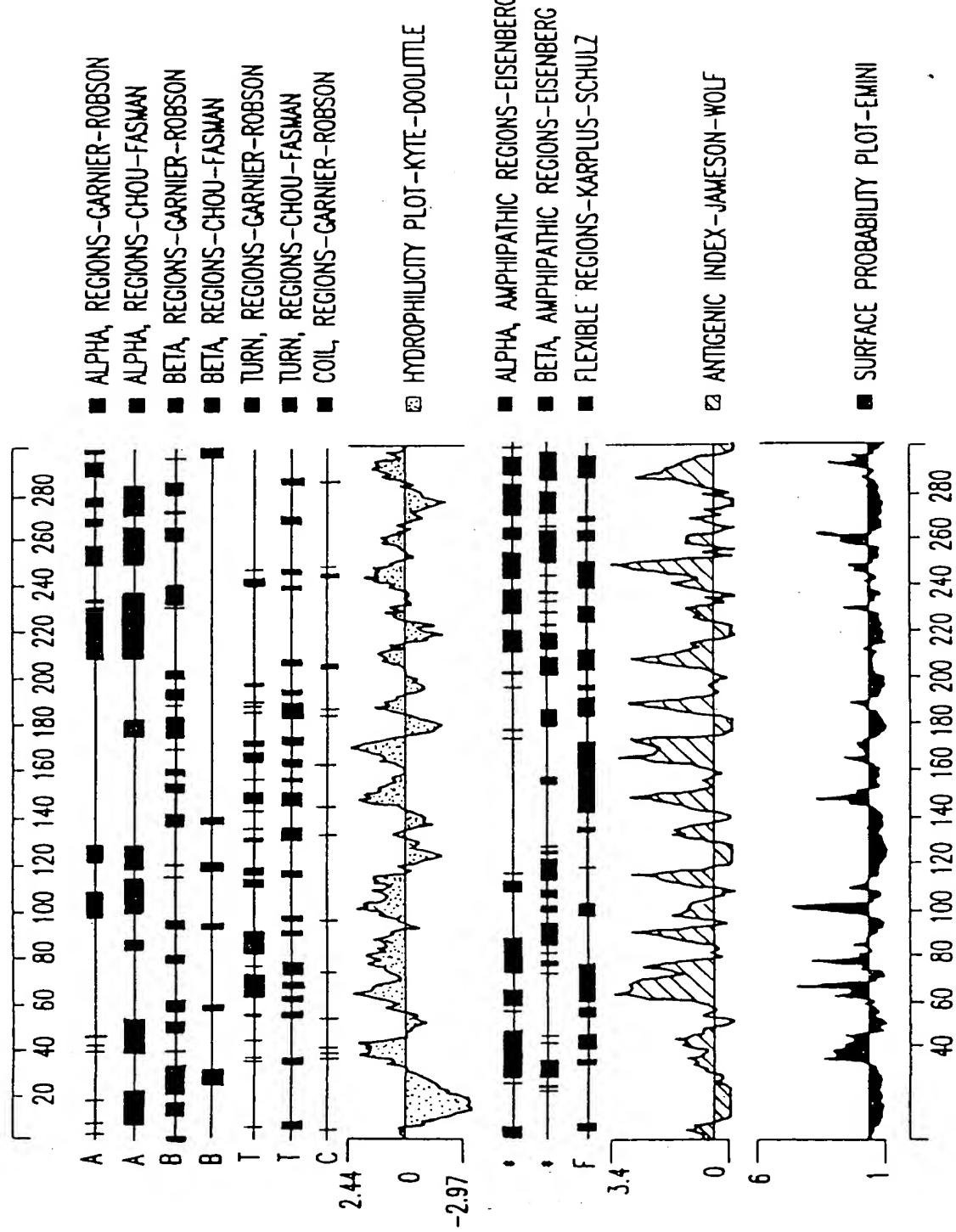
FIG. 3N

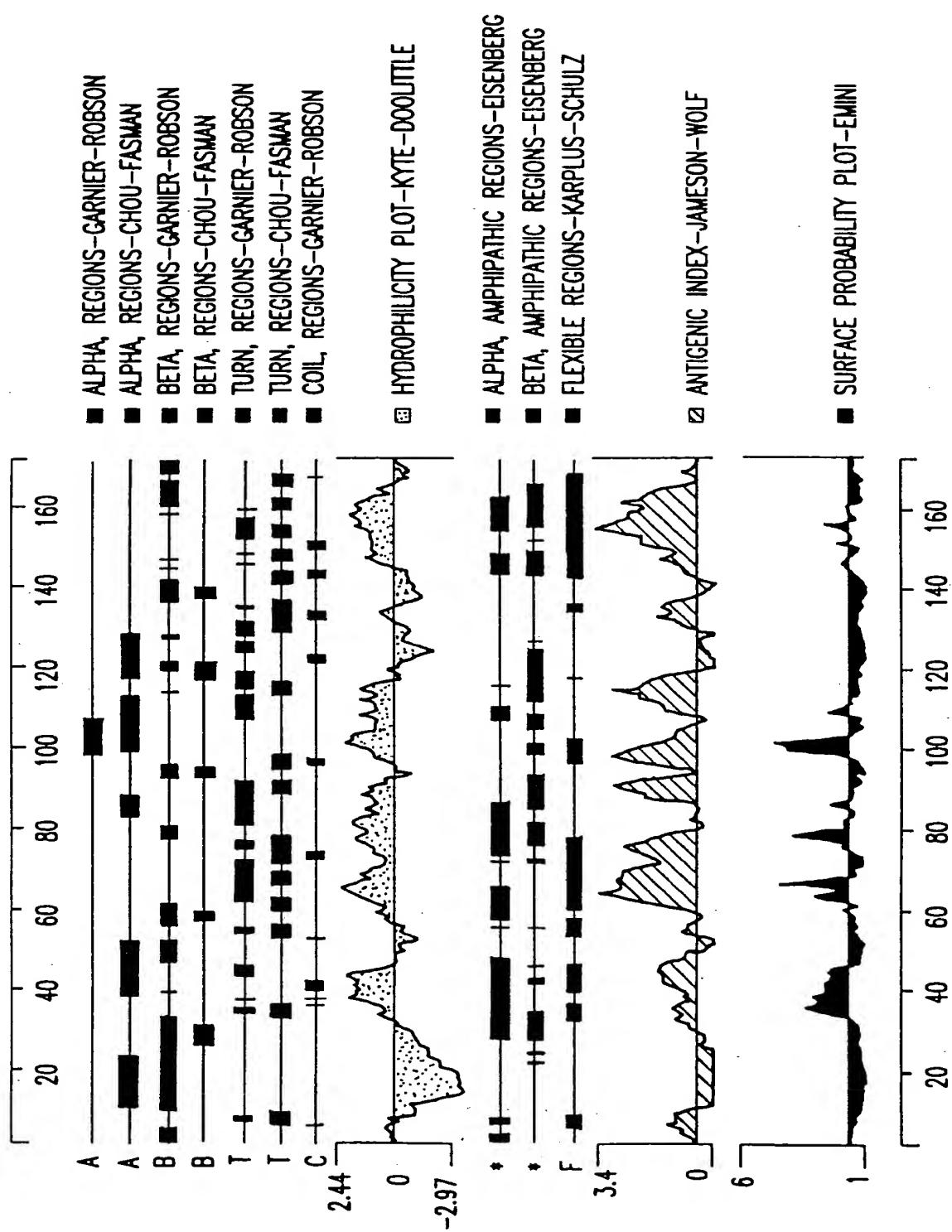
434	- - - - - L E D I E E A L C G P A A L P - - - - -	- - - - - R S Q L E T P E T L L G S T E K TNFR1
431	- - - - -	- - - - - L A A L R R I Q R A D TNFR2
401	- - - - -	- - - - - P G P S E L S T P Y Q E D G K A W NGFR
386	- - - - -	- - - - -
312	- - - - - T I I L K D I T S D - S E N S N F R - - - - -	- - - - -
246	- - - - -	- - - - -
520	M K A D T V I V G T V K A E L P E G R G L A G P A E P E L E E E L E A D H T P H CD30	- - - - - Q E D G K E S CD40
263	- - - - -	- - - - -
224	F K - - - - -	- - - - - Q P F M R P V Q T T 4-1BB
260	- - - - -	- - - - -
345	- - - - -	- - - - - R T P 0X40
351	- - - - -	- - - - -
291	- - - - -	- - - - - VC22
163	- - - - -	- - - - - CRMβ
	- - - - -	- - - - - SV R E R TNFR-6α
	- - - - -	- - - - - VA G P S TNFR-6β

449	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	P A P S L L R	TNFR1
448	P - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	L P L G V P D A G M K P S	TNFR2
413	L V E S L C S E S	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- T A T S P V	NGFR
403	H - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	L A E T - E T L G C Q D L	LTbR
329	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- N E I Q S L V	FAS
247	I Q E D - Y R K P	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- E P A C S P	CD27
560	Y P E Q E T E P P L G S C S D V	M L S V E E E G K E D P L	P T A A S G K	C D 30	C D 40	C D 40	C D 40	C D 40
270	R - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	I S V Q - E R Q	CD40
236	Q E E D G C	- - - S C	- - - R F P E E E G	- - - - -	- - - - -	- - - - -	- G C E L	4-1BB
263	I Q E E Q A D A H	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- S T L A K I	OX40
349	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- L	VC22
355	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- L	CRMB
296	F - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- H	TNFR-6a
168	L - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- A P	TNFR-6b

FIG.3P

FIG. 4





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**HELDI06R**

GGCACCGAGCA GGGTCCTGTN TCCGCCCTGA GCCGCGCTCT NCCTGCTCCA GCAAGGACCA  
TGAGGGCGCT GGAGGGGCCA GGCGCTGCGC TGCTGTGCCT GGTGTTGGCG CTGCCTGCC  
TGCTGCCGGT GCCGGCTGTA CGCGGAGTGG CAGAAACACN NACNTACCCC TGGCGGGACG  
NAGAGACAGG GGAGCGGCTG GTGTNTNCCC ANTGCCCCCC AGGCACCTTT NTGCAGCGGC  
CGTGCCGNCG AGACAGCCCC ACGACGTGTG GCCCGTNTCC ACCGCGCCAC TACACGCATT  
CTGGAACTAC CTGGAGCGCT GNCGTTACTN CAACGTCTC TGCGGGGAGC GTNAGGAGGA  
GGCACGGGTT TNCCACGNCA ACCACAACCG NGGNNTTACCG TNGCCGNACC GGTTTCTTCG  
NGGCAAGTTG GTTTTNNTT TGGAGNAAGG ATTGTGTTN CAATTNATTG ACGNAGTGAT  
TNNNCNCGGG AAACTNAAA

**HCEOW38R**

CGCAACTGCA CGGCCCTGGG ACTGGCCCTC AATGTGCCAG GNTCTTCCTC CCATGACACC  
CTGTGCACCA GCTGCACTGG CTTCCCCCTC AGCACCAAGGG TACCANGAGC TGAGGAGTGT  
GAGCNTGCCG TCATCGACTT TTTGGCTTTC CAGGACATCT CCATCAAGAG GCTGCAGCGG  
CTGCTCANGC C

**FIG.6**

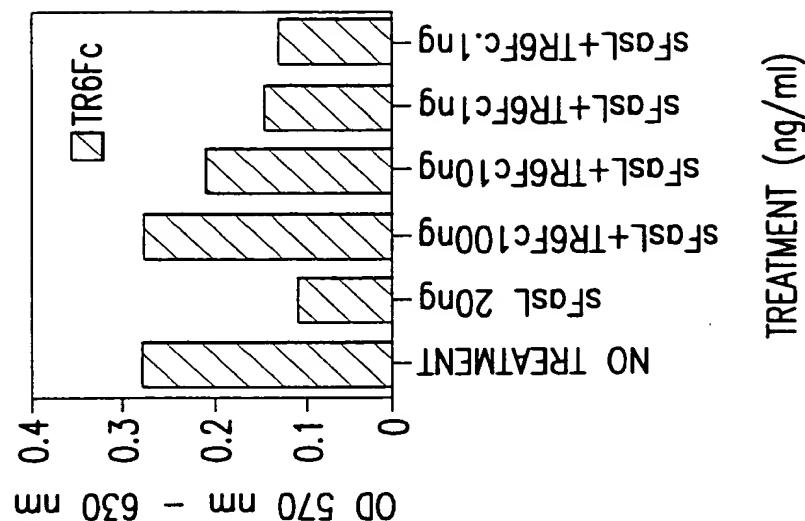


FIG. 7B

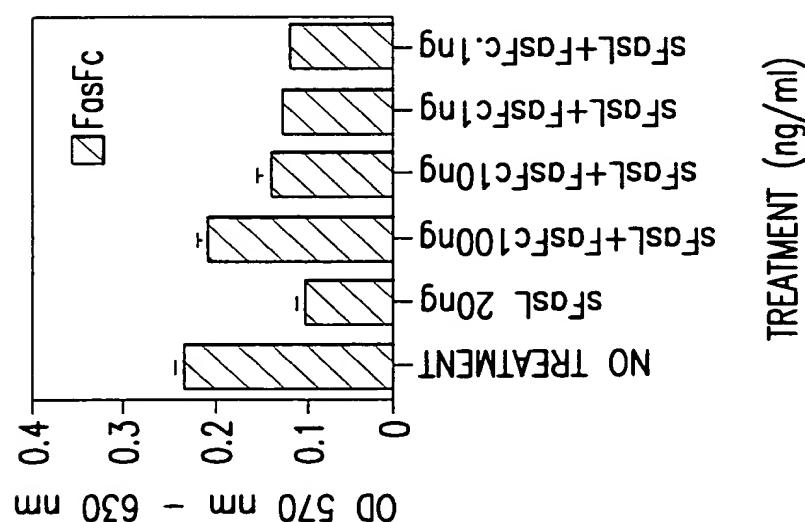


FIG. 7A